

Figure 1:
ATRX open reading frame (SEQ ID NO:1) and translation to corresponding polypeptide (SEQ ID NO:2)

1	ATG	ACC	GCT	GAG	CCC	ATG	AGT	GAA	AGC	AAG	TTG	AAT	ACA	TTG	GTG	45
1	M	T	A	E	P	M	S	E	S	K	L	N	T	L	V	15
46	CAG	AAG	CTT	CAT	GAC	TTC	CTT	GCA	CAC	TCA	TCA	GAA	GAA	TCT	GAA	90
16	Q	K	L	H	D	F	L	A	H	S	S	E	E	S	E	30
91	GAA	ACA	AGT	TCT	CCT	CCA	CGA	CTT	GCA	ATG	AAT	CAA	AAC	ACA	GAT	135
31	E	T	S	S	P	P	R	L	A	M	N	Q	N	T	D	45
136	AAA	ATC	AGT	GGT	TCT	GGA	AGT	AAC	TCT	GAT	ATG	ATG	GAA	AAC	AGC	180
46	K	I	S	G	S	G	S	N	S	D	M	M	E	N	S	60
181	AAG	GAA	GAG	GGA	ACT	AGC	TCT	TCA	GAA	AAA	TCC	AAG	TCT	TCA	GGA	225
61	K	E	E	G	T	S	S	S	E	K	S	K	S	S	G	75
226	TCG	TCA	CGA	TCA	AAG	AGG	AAA	CCT	TCA	ATT	GTA	ACA	AAG	TAT	GTA	270
76	S	S	R	S	K	R	K	P	S	I	V	T	K	Y	V	90
271	GAA	TCA	GAT	GAT	GAA	AAA	CCT	TTG	GAT	GAT	GAA	ACT	GTA	AAT	GAA	315
91	E	S	D	D	E	K	P	L	D	D	E	T	V	N	E	105
316	GAT	GCG	TCT	AAT	GAA	AAT	TCA	GAA	AAT	GAT	ATT	ACT	ATG	CAG	AGC	360
106	D	A	S	N	E	N	S	E	N	D	I	T	M	Q	S	120
361	TTG	CCA	AAA	GGT	ACA	GTG	ATT	GTA	CAG	CCA	GAG	CCA	GTG	CTG	AAT	405
121	L	P	K	G	T	V	I	V	Q	P	E	P	V	L	N	135
406	GAA	GAC	AAA	GAT	GAT	TTT	AAA	GGG	CCT	GAA	TTT	AGA	AGC	AGA	AGT	450
136	E	D	K	D	D	F	K	G	P	E	F	R	S	R	S	150
451	AAA	ATG	AAA	ACT	GAA	AAT	CTC	AAA	AAA	CGC	GGA	GAA	GAT	GGG	CTT	495
151	K	M	K	T	E	N	L	K	K	R	G	E	D	G	L	165
496	CAT	GGG	ATT	GTG	AGC	TGC	ACT	GCT	TGT	GGA	CAA	CAG	GTC	AAT	CAT	540
166	H	G	I	V	S	C	T	A	C	G	Q	Q	V	N	H	180
541	TTT	CAA	AAA	GAT	TCC	ATT	TAT	AGA	CAC	CCT	TCA	TTG	CAA	GTT	CTT	585
181	F	Q	K	D	S	I	Y	R	H	P	S	L	Q	V	L	195
586	ATT	TGT	AAG	AAT	TGC	TTT	AAG	TAT	TAC	ATG	AGT	GAT	GAT	ATT	AGC	630
196	I	C	K	N	C	F	K	Y	Y	M	S	D	D	I	S	210
631	CGT	GAC	TCA	GAT	GGA	ATG	GAT	GAA	CAA	TGT	AGG	TGG	TGT	GCG	GAA	675
211	R	D	S	D	G	M	D	E	Q	C	R	W	C	A	E	225
676	GGT	GGA	AAC	TTG	ATT	TGT	TGT	GAC	TTT	TGC	CAT	AAT	GCT	TTC	TGC	720
226	G	G	N	L	I	C	C	D	F	C	H	N	A	F	C	240
721	AAG	AAA	TGC	ATT	CTA	CGC	AAC	CTT	GGT	CGA	AAG	GAG	TTG	TCC	ACA	765
241	K	K	C	I	L	R	N	L	G	R	K	E	L	S	T	255
766	ATA	ATG	GAT	GAA	AAC	AAC	CAA	TGG	TAT	TGC	TAC	ATT	TGT	CAC	CCA	810
256	I	M	D	E	N	N	Q	W	Y	C	Y	I	C	H	P	270
811	GAG	CCT	TTG	TTG	GAC	TTG	GTC	ACT	GCA	TGT	AAC	AGC	GTA	TTT	GAG	855
271	E	P	L	L	D	L	V	T	A	C	N	S	V	F	E	285
856	AAT	TTA	GAA	CAG	TTG	TTG	CAG	CAA	AAT	AAG	AAG	AAG	ATA	AAA	GTT	900

286	N	L	E	Q	L	L	Q	Q	N	K	K	K	I	K	V	300
901	GAC	AGT	GAA	AAG	AGT	AAT	AAA	GTA	TAT	GAA	CAT	ACA	TCC	AGA	TTT	945
301	D	S	E	K	S	N	K	V	Y	E	H	T	S	R	F	315
946	TCT	CCA	AAG	AAG	ACT	AGT	TCA	AAT	TGT	AAT	GGA	GAA	GAA	AAG	AAA	990
316	S	P	K	K	T	S	S	N	C	N	G	E	E	K	K	330
991	TTA	GAT	GAT	TCC	TGT	TCT	GGC	TCT	GTA	ACC	TAC	TCT	TAT	TCC	GCA	1035
331	L	D	D	S	C	S	G	S	V	T	Y	S	Y	S	A	345
1036	CTA	ATT	GTG	CCC	AAA	GAG	ATG	ATT	AAG	AAG	GCA	AAA	AAA	CTG	ATT	1080
346	L	I	V	P	K	E	M	I	K	K	A	K	K	L	I	360
1081	GAG	ACC	ACA	GCC	AAC	ATG	AAC	TCC	AGT	TAT	GTT	AAA	TTT	TTA	AAG	1125
361	E	T	T	A	N	M	N	S	S	Y	V	K	F	L	K	375
1126	CAG	GCA	ACA	GAT	AAT	TCA	GAA	ATC	AGT	TCT	GCT	ACA	AAA	TTA	CGT	1170
376	Q	A	T	D	N	S	E	I	S	S	A	T	K	L	R	390
1171	CAG	CTT	AAG	GCT	TTT	AAG	TCT	GTG	TTG	GCT	GAT	ATT	AAG	AAG	GCT	1215
391	Q	L	K	A	F	K	S	V	L	A	D	I	K	K	A	405
1216	CAT	CTT	GCA	TTG	GAA	GAA	GAC	TTA	AAT	TCC	GAG	TTT	CGA	GCG	ATG	1260
406	H	L	A	L	E	E	D	L	N	S	E	F	R	A	M	420
1261	GAT	GCT	GTA	AAC	AAA	GAG	AAA	AAT	ACC	AAA	GAG	CAT	AAA	GTC	ATA	1305
421	D	A	V	N	K	E	K	N	T	K	E	H	K	V	I	435
1306	GAT	GCT	AAG	TTT	GAA	ACA	AAA	GCA	CGA	AAA	GGA	GAA	AAA	CCT	TGT	1350
436	D	A	K	F	E	T	K	A	R	K	G	E	K	P	C	450
1351	GCT	TTG	GAA	AAG	AAG	GAT	ATT	TCA	AAG	TCA	GAA	GCT	AAA	CTT	TCA	1395
451	A	L	E	K	K	D	I	S	K	S	E	A	K	L	S	465
1396	AGA	AAA	CAG	GTA	GAT	AGT	GAG	CAC	ATG	CAT	CAG	AAT	GTT	CCA	ACA	1440
466	R	K	Q	V	D	S	E	H	M	H	Q	N	V	P	T	480
1441	GAG	GAA	CAA	AGA	ACA	AAT	AAA	AGY	ACC	GGT	GGT	GAA	CAT	AAG	AAA	1485
481	E	E	Q	R	T	N	K	X	T	G	G	E	H	K	K	495
1486	TCT	GAT	AGA	AAA	GAA	GAA	CCT	CAA	TAT	GAA	CCT	GCC	AAC	ACT	TCT	1530
496	S	D	R	K	E	E	P	Q	Y	E	P	A	N	T	S	510
1531	GAA	GAT	TTA	GAC	ATG	GAT	ATT	GTG	TCT	GTT	CCT	TCC	TCA	GTT	CCA	1575
511	E	D	L	D	M	D	I	V	S	V	P	S	S	V	P	525
1576	GAA	GAC	ATT	TTT	GAG	AAT	CTT	GAG	ACT	GCT	ATG	GAA	GTT	CAG	AGT	1620
526	E	D	I	F	E	N	L	E	T	A	M	E	V	Q	S	540
1621	TCA	GTT	GAT	CAT	CAA	GGG	GAT	GGC	AGC	AGT	GGA	ACT	GAA	CAA	GAA	1665
541	S	V	D	H	Q	G	D	G	S	S	G	T	E	Q	E	555
1666	GTG	GAG	AGT	TCA	TCT	GTA	AAA	TTA	AAT	ATT	TCT	TCA	AAA	GAC	AAC	1710
556	V	E	S	S	S	V	K	L	N	I	S	S	K	D	N	570
1711	AGA	GGA	GGT	ATT	AAA	TCA	AAA	ACT	ACA	GCT	AAA	GTA	ACA	AAA	GAA	1755
571	R	G	G	I	K	S	K	T	T	A	K	V	T	K	E	585
1756	TTA	TAT	GTT	AAA	CTC	ACT	CCT	GTT	TCC	CTT	CCT	AAT	TCC	CCA	ATT	1800
586	L	Y	V	K	L	T	P	V	S	L	P	N	S	P	I	600
1801	AAA	GGT	GCT	GAT	TGT	CAG	GAA	GTT	CCA	CAA	GAT	AAA	GAT	GGC	TAT	1845
601	K	G	A	D	C	Q	E	V	P	Q	D	K	D	G	Y	615

1846	AAA AGT TGT GGT CTG AAC CCC AAG TTA GAG AAA TGT GGA CTT GGA	1890
616	K S C G L N P K L E K C G L G	630
1891	CAG GAA AAC AGT GAT AAT GAG CAT TTG GTT GAA AAT GAA GTT TCA	1935
631	Q E N S D N E H L V E N E V S	645
1936	TTA CTT TTA GAG GAA TCT GAT CTT CGG AGA TCC CCA CGT GTA AAG	1980
646	L L L E E S D L R R S P R V K	660
1981	ACT ACA CCC TTG AGG CGA CCG ACA GAA ACT AAC CCT GTA ACA TCT	2025
661	T T P L R R P T E T N P V T S	675
2026	AAT TCA GAT GAA GAA TGT AAT GAA ACA GTT AAG GAG AAA CAA AAA	2070
676	N S D E E C N E T V K E K Q K	690
2071	CTA TCA GTT CCA GTG AGA AAA AAG GAT AAG CGT AAT TCT TCT GAC	2115
691	L S V P V R K K D K R N S S D	705
2116	AGT GCT ATA GAT AAT CCT AAG CCT AAT AAA TTG CCA AAA TCT AAG	2160
706	S A I D N P K P N K L P K S K	720
2161	CAA TCA GAG ACT GTG GAT CAA AAT TCA GAT TCT GAT GAA ATG CTA	2205
721	Q S E T V D Q N S D S D E M L	735
2206	GCA ATC CTC AAA GGG GTG AGC AGG ATG AGT CAC AGT TCT TCT TCA	2250
736	A I L K G V S R M S H S S S S	750
2251	GAT ACT GAT ATT AAT GAA ATT CAT ACA AAC CAT AAG ACT TTG TAT	2295
751	D T D I N E I H T N H K T L Y	765
2296	GAT TTA AAG ACT CAG GCG GGG AAA GAT GAT AAA GGA AAA AGG AAA	2340
766	D L K T Q A G K D D K G K R K	780
2341	CGA AAA AGT TCT ACA TCT GGC TCA GAT TTT GAT ACT AAA AAG GGC	2385
781	R K S S T S G S D F D T K K G	795
2386	AAA TCA GCT AAG AGC TCT ATA ATT TCT AAA AAG AAA CGA CAA ACC	2430
796	K S A K S S I I S K K K R Q T	810
2431	CAG TCT GAG TCT TCT AAT TAT GAC TCA GAA TTA GAA AAA GAG ATA	2475
811	Q S E S S N Y D S E L E K E I	825
2476	AAG AGC ATG AGT AAA ATT GGT GCT GCC AGA ACC ACC AAA AAA AGA	2520
826	K S M S K I G A A R T T K K R	840
2521	ATT CCA AAT ACA AAA GAT TTT GAC TCT TCT GAA GAT GAG AAA CAC	2565
841	I P N T K D F D S S E D E K H	855
2566	AGC AAA AAA GGA ATG GAT AAT CAA GGG CAC AAA AAT TTG AAG ACC	2610
856	S K K G M D N Q G H K N L K T	870
2611	TCA CAA GAA GGA TCA TCT GAT GAT GCT GAA AGA AAA CAA GAG AGA	2655
871	S Q E G S S D D A E R K Q E R	885
2656	GAG ACT TTC TCT TCA GCA GAA GGC ACA GTT GAT AAA GAC ACG ACC	2700
886	E T F S S A E G T V D K D T T	900
2701	ATC ATG GAA TTA AGA GAT CGA CTT CCT AAG AAG CAG CAA GCA AGT	2745
901	I M E L R D R L P K K Q Q A S	915
2746	GCT TCC ACT GAT GGT GTC GAT AAG CTT TCT GGG AAA GAG CAG AGT	2790
916	A S T D G V D K L S G K E Q S	930
2791	TTT ACT TCT TTG GAA GTT AGA AAA GTT GCT GAA ACT AAA GAA AAG	2835
931	F T S L E V R K V A E T K E K	945

2836	AGC	AAG	CAT	CTC	AAA	ACC	AAA	ACA	TGT	AAA	AAA	GTA	CAG	GAT	GGC	2880
946	S	K	H	L	K	T	K	T	C	K	K	V	Q	D	G	960
2881	TTA	TCT	GAT	ATT	GCA	GAG	AAA	TTC	CTA	AAG	AAA	GAC	CAG	AGC	GAT	2925
961	L	S	D	I	A	E	K	F	L	K	K	D	Q	S	D	975
2926	GAA	ACT	TCT	GAA	GAT	GAT	AAA	AAG	CAG	AGC	AAA	AAG	GGA	ACT	GAA	2970
976	E	T	S	E	D	D	K	K	Q	S	K	K	G	T	E	990
2971	GAA	AAA	AAG	AAA	CCT	TCA	GAC	TTT	AAG	AAA	AAA	GTA	ATT	AAA	ATG	3015
991	E	K	K	K	P	S	D	F	K	K	K	V	I	K	M	1005
3016	GAA	CAA	CAG	TAT	GAA	TCT	TCA	TCT	GAT	GGC	ACT	GAA	AAG	TTA	CCT	3060
1006	E	Q	Q	Y	E	S	S	S	D	G	T	E	K	L	P	1020
3061	GAG	CGA	GAA	GAA	ATT	TGT	CAT	TTT	CCT	AAG	GGC	ATA	AAA	CAA	ATT	3105
1021	E	R	E	E	I	C	H	F	P	K	G	I	K	Q	I	1035
3106	AAG	AAT	GGA	ACA	ACT	GAT	GGA	GAA	AAG	AAA	AGT	AAA	AAA	ATA	AGA	3150
1036	K	N	G	T	T	D	G	E	K	K	S	K	K	I	R	1050
3151	GAT	AAA	ACT	TCT	AAA	AAG	AAG	GAT	GAA	TTA	TCT	GAT	TAT	GCT	GAG	3195
1051	D	K	T	S	K	K	K	D	E	L	S	D	Y	A	E	1065
3196	AAG	TCA	ACA	GGG	AAA	GGA	GAT	AGT	TGT	GAC	TCT	TCA	GAG	GAT	AAA	3240
1066	K	S	T	G	K	G	D	S	C	D	S	S	E	D	K	1080
3241	AAG	AGT	AAG	AAT	GGA	GCA	TAT	GGT	AGA	GAG	AAG	AAA	AGG	TGC	AAG	3285
1081	K	S	K	N	G	A	Y	G	R	E	K	K	R	C	K	1095
3286	TTG	CTT	GGA	AAG	AGT	TCA	AGG	AAG	AGA	CAA	GAT	TGC	TCA	TCA	TCT	3330
1096	L	L	G	K	S	S	R	K	R	Q	D	C	S	S	S	1110
3331	GAT	ACT	GAG	AAA	TAT	TCC	ATG	AAA	GAA	GAT	GGT	TGT	AAC	TCT	TCT	3375
1111	D	T	E	K	Y	S	M	K	E	D	G	C	N	S	S	1125
3376	GAT	AAG	AGA	CTG	AAA	AGA	ATA	GAA	TTG	AGG	GAA	AGA	AGA	AAT	TTA	3420
1126	D	K	R	L	K	R	I	E	L	R	E	R	R	N	L	1140
3421	AGT	TCA	AAG	AGA	AAT	ACT	AAG	GAA	ATA	CAA	AGT	GGC	TCA	TCA	TCA	3465
1141	S	S	K	R	N	T	K	E	I	Q	S	G	S	S	S	1155
3466	TCT	GAT	GCT	GAG	GAA	AGT	TCT	GAA	GAT	AAT	AAA	AAG	AAG	AAG	CAA	3510
1156	S	D	A	E	E	S	S	E	D	N	K	K	K	K	Q	1170
3511	AGA	ACT	TCA	TCT	AAA	AAG	AAG	GCA	GTC	ATT	GTC	AAG	GAG	AAA	AAG	3555
1171	R	T	S	S	K	K	K	A	V	I	V	K	E	K	K	1185
3556	AGA	AAC	TCC	CTA	AGA	ACA	AGC	ACT	AAA	AGG	AAG	CAA	GCT	GAC	ATT	3600
1186	R	N	S	L	R	T	S	T	K	R	K	Q	A	D	I	1200
3601	ACA	TCC	TCA	TCT	TCT	TCT	GAT	ATA	GAA	GAT	GAT	GAT	CAG	AAT	TCT	3645
1201	T	S	S	S	S	S	D	I	E	D	D	D	Q	N	S	1215
3646	ATA	GGT	GAG	GGA	AGC	AGC	GAT	GAA	CAG	AAA	ATT	AAG	CCT	GTC	ACT	3690
1216	I	G	E	G	S	S	D	E	Q	K	I	K	P	V	T	1230
3691	GAA	AAT	TTA	GTG	CTG	TCT	TCA	CAT	ACT	GGA	TTT	TGC	CAA	TCT	TCA	3735
1231	E	N	L	V	L	S	S	H	T	G	F	C	Q	S	S	1245
3736	GGA	GAT	GAA	GCC	TTA	TCT	AAA	TCA	GTG	CCT	GTC	ACA	GTG	GAT	GAT	3780
1246	G	D	E	A	L	S	K	S	V	P	V	T	V	D	D	1260
3781	GAT	GAT	GAC	GAC	AAT	GAT	CCT	GAG	AAT	AGA	ATT	GCC	AAG	AAG	ATG	3825

1261	D	D	D	D	N	D	P	E	N	R	I	A	K	K	M	1275
3826	CTT	TTA	GAA	GAA	ATT	AAA	GCC	AAT	CTT	TCC	TCT	GAT	GAG	GAT	GGA	3870
1276	L	L	E	E	I	K	A	N	L	S	S	D	E	D	G	1290
3871	TCT	TCA	GAT	GAT	GAG	CCA	GAA	GAA	GGG	AAA	AAA	AGA	ACT	GGA	AAA	3915
1291	S	S	D	D	E	P	E	E	G	K	K	R	T	G	K	1305
3916	CAA	AAT	GAA	GAA	AAC	CCA	GGA	GAT	GAG	GAA	GCA	AAA	AAT	CAA	GTC	3960
1306	Q	N	E	E	N	P	G	D	E	E	A	K	N	Q	V	1320
3961	AAT	TCT	GAA	TCA	GAT	TCA	GAT	TCT	GAA	GAA	TCT	AAG	AAG	CCA	AGA	4005
1321	N	S	E	S	D	S	D	S	E	E	S	K	K	P	R	1335
4006	TAC	AGA	CAT	AGG	CTT	TTG	CGG	CAC	AAA	TTG	ACT	GTG	AGT	GAC	GGA	4050
1336	Y	R	H	R	L	L	R	H	K	L	T	V	S	D	G	1350
4051	GAA	TCT	GGA	GAA	GAA	AAA	AAG	ACA	AAG	CCT	AAA	GAG	CAT	AAA	GAA	4095
1351	E	S	G	E	E	K	K	T	K	P	K	E	H	K	E	1365
4096	GTC	AAA	GGC	AGA	AAC	AGA	AGA	AAG	GTG	AGC	AGT	GAA	GAT	TCA	GAA	4140
1366	V	K	G	R	N	R	R	K	V	S	S	E	D	S	E	1380
4141	GAT	TCT	GAT	TTT	CAG	GAA	TCA	GGA	GTT	AGT	GAA	GAA	GTT	AGT	GAA	4185
1381	D	S	D	F	Q	E	S	G	V	S	E	E	V	S	E	1395
4186	TCC	GAA	GAT	GAA	CAG	CGG	CCC	AGA	ACA	AGG	TCT	GCA	AAG	AAA	GCA	4230
1396	S	E	D	E	Q	R	P	R	T	R	S	A	K	K	A	1410
4231	GAG	TTG	GAA	GAA	AAT	CAG	CGG	AGC	TAT	AAA	CAG	AAA	AAG	AAA	AGG	4275
1411	E	L	E	E	N	Q	R	S	Y	K	Q	K	K	K	R	1425
4276	CGA	CGT	ATT	AAG	GTT	CAA	GAA	GAT	TCA	TCC	AGT	GAA	AAC	AAG	AGT	4320
1426	R	R	I	K	V	Q	E	D	S	S	S	E	N	K	S	1440
4321	AAT	TCT	GAG	GAA	GAA	GAG	GAG	GAA	AAA	GAA	GAG	GAG	GAG	GAA	GAG	4365
1441	N	S	E	E	E	E	E	E	K	E	E	E	E	E	E	1455
4366	GAG	GAG	GAG	GAG	GAA	GAG	GAG	GAG	GAA	GAT	GAA	AAT	GAT	GAT	TCC	4410
1456	E	E	E	E	E	E	E	E	E	D	E	N	D	D	S	1470
4411	AAG	TCT	CCT	GGA	AAA	GGC	AGA	AAG	AAA	ATT	CGG	AAG	ATT	CTT	AAA	4455
1471	K	S	P	G	K	G	R	K	K	I	R	K	I	L	K	1485
4456	GAT	GAT	AAA	CTG	AGA	ACA	GAA	ACA	CAA	AAT	GCT	CTT	AAG	GAA	GAG	4500
1486	D	D	K	L	R	T	E	T	Q	N	A	L	K	E	E	1500
4501	GAA	GAG	AGA	CGA	AAA	CGT	ATT	GCT	GAG	AGG	GAG	CGT	GAG	CGA	GAA	4545
1501	E	E	R	R	K	R	I	A	E	R	E	R	E	R	E	1515
4546	AAA	TTG	AGA	GAG	GTG	ATA	GAA	ATT	GAA	GAT	GCT	TCA	CCC	ACC	AAG	4590
1516	K	L	R	E	V	I	E	I	E	D	A	S	P	T	K	1530
4591	TGT	CCA	ATA	ACA	ACC	AAG	TTG	GTT	TTA	GAT	GAA	GAT	GAA	GAA	ACC	4635
1531	C	P	I	T	T	K	L	V	L	D	E	D	E	E	T	1545
4636	AAA	GAA	CCT	TTA	GTG	CAG	GTT	CAT	AGA	AAT	ATG	GTT	ATC	AAA	TTG	4680
1546	K	E	P	L	V	Q	V	H	R	N	M	V	I	K	L	1560
4681	AAA	CCC	CAT	CAA	GTA	GAT	GGT	GTT	CAG	TTT	ATG	TGG	GAT	TGC	TGC	4725
1561	K	P	H	Q	V	D	G	V	Q	F	M	W	D	C	C	1575
4726	TGT	GAG	TCT	GTG	AAA	AAA	ACA	AAG	AAA	TCT	CCA	GGT	TCA	GGA	TGC	4770
1576	C	E	S	V	K	K	T	K	K	S	P	G	S	G	C	1590

4771	ATT	CTT	GCC	CAC	TGT	ATG	GGC	CTT	GGT	AAG	ACT	TTA	CAG	GTG	GTA	4815
1591	I	L	A	H	C	M	G	L	G	K	T	L	Q	V	V	1605
4816	AGT	TTT	CTT	CAT	ACA	GTT	CTT	TTG	TGT	GAC	AAA	CTG	GAT	TTC	AGC	4860
1606	S	F	L	H	T	V	L	L	C	D	K	L	D	F	S	1620
4861	ACG	GCG	TTA	GTG	GTT	TGT	CCT	CTT	AAT	ACT	GCT	TTG	AAT	TGG	ATG	4905
1621	T	A	L	V	V	C	P	L	N	T	A	L	N	W	M	1635
4906	AAT	GAA	TTT	GAG	AAG	TGG	CAA	GAG	GGA	TTA	AAA	GAT	GAT	GAG	AAG	4950
1636	N	E	F	E	K	W	Q	E	G	L	K	D	D	E	K	1650
4951	CTT	GAG	GTT	TCT	GAA	TTA	GCA	ACT	GTG	AAA	CGT	CCT	CAG	GAG	AGA	4995
1651	L	E	V	S	E	L	A	T	V	K	R	P	Q	E	R	1665
4996	AGC	TAC	ATG	CTG	CAG	AGG	TGG	CAA	GAA	GAT	GGT	GGT	GTT	ATG	ATC	5040
1666	S	Y	M	L	Q	R	W	Q	E	D	G	G	V	M	I	1680
5041	ATA	GGC	TAT	GAG	ATG	TAT	AGA	AAT	CTT	GCT	CAA	GGA	AGG	AAT	GTG	5085
1681	I	G	Y	E	M	Y	R	N	L	A	Q	G	R	N	V	1695
5086	AAG	AGT	CGG	AAA	CTT	AAA	GAA	ATA	TTT	AAC	AAA	GCT	TTG	GTT	GAT	5130
1696	K	S	R	K	L	K	E	I	F	N	K	A	L	V	D	1710
5131	CCA	GGC	CCT	GAT	TTT	GTT	GTT	TGT	GAT	GAA	GGC	CAT	ATT	CTA	AAA	5175
1711	P	G	P	D	F	V	V	C	D	E	G	H	I	L	K	1725
5176	AAT	GAA	GCA	TCT	GCT	GTT	TCT	AAA	GCT	ATG	AAT	TCT	ATA	CGA	TCA	5220
1726	N	E	A	S	A	V	S	K	A	M	N	S	I	R	S	1740
5221	AGG	AGG	AGG	ATT	ATT	TTA	ACA	GGA	ACA	CCA	CTT	CAA	AAT	AAC	CTA	5265
1741	R	R	R	I	I	L	T	G	T	P	L	Q	N	N	L	1755
5266	ATT	GAG	TAT	CAT	TGT	ATG	GTT	AAT	TTT	ATC	AAG	GAA	AAT	TTA	CTT	5310
1756	I	E	Y	H	C	M	V	N	F	I	K	E	N	L	L	1770
5311	GGA	TCC	ATT	AAG	GAG	TTC	AGG	AAT	AGA	TTT	ATA	AAT	CCA	ATT	CAA	5355
1771	G	S	I	K	E	F	R	N	R	F	I	N	P	I	Q	1785
5356	AAT	GGT	CAG	TGT	GCA	GAT	TCT	ACC	ATG	GTA	GAT	GTC	AGA	GTG	ATG	5400
1786	N	G	Q	C	A	D	S	T	M	V	D	V	R	V	M	1800
5401	AAA	AAA	CGT	GCT	CAC	ATT	CTC	TAT	GAG	ATG	TTA	GCT	GGA	TGT	GTT	5445
1801	K	K	R	A	H	I	L	Y	E	M	L	A	G	C	V	1815
5446	CAG	AGG	AAA	GAT	TAT	ACA	GCA	TTA	ACA	AAA	TTC	TTG	CCT	CCA	AAA	5490
1816	Q	R	K	D	Y	T	A	L	T	K	F	L	P	P	K	1830
5491	CAC	GAA	TAT	GTG	TTA	GCT	GTG	AGA	ATG	ACT	TCT	ATT	CAG	TGC	AAG	5535
1831	H	E	Y	V	L	A	V	R	M	T	S	I	Q	C	K	1845
5536	CTC	TAT	CAG	TAC	TAC	TTA	GAT	CAC	TTA	ACA	GGT	GTG	GGC	AAT	AAT	5580
1846	L	Y	Q	Y	Y	L	D	H	L	T	G	V	G	N	N	1860
5581	AGT	GAA	GGT	GGA	AGA	GGA	AAG	GCA	GGT	GCA	AAG	CTT	TTC	CAA	GAT	5625
1861	S	E	G	G	R	G	K	A	G	A	K	L	F	Q	D	1875
5626	TTT	CAG	ATG	TTA	AGT	AGA	ATA	TGG	ACT	CAT	CCT	TGG	TGT	TTG	CAG	5670
1876	F	Q	M	L	S	R	I	W	T	H	P	W	C	L	Q	1890
5671	CTA	GAC	TAC	ATT	AGC	AAA	GAA	AAT	AAG	GGT	TAT	TTT	GAT	GAA	GAC	5715
1891	L	D	Y	I	S	K	E	N	K	G	Y	F	D	E	D	1905
5716	AGT	ATG	GAT	GAA	TTT	ATA	GCC	TCA	GAT	TCT	GAT	GAA	ACC	TCC	ATG	5760
1906	S	M	D	E	F	I	A	S	D	S	D	E	T	S	M	1920

5761	AGT	TTA	AGC	TCC	GAT	GAT	TAT	ACA	AAA	AAG	AAG	AAA	AAA	GGG	AAA	5805
1921	S	L	S	S	D	D	Y	T	K	K	K	K	K	G	K	1935
5806	AAG	GGG	AAA	AAA	GAT	AGT	AGC	TCA	AGT	GGA	AGT	GGC	AGT	GAC	AAT	5850
1936	K	G	K	K	D	S	S	S	S	G	S	G	S	D	N	1950
5851	GAT	GTT	GAA	GTG	ATT	AAG	GTC	TGG	AAT	TCA	AGA	TCT	CGG	GGA	GGT	5895
1951	D	V	E	V	I	K	V	W	N	S	R	S	R	G	G	1965
5896	GGT	GAA	GGA	AAT	GTG	GAT	GAA	ACA	GGA	AAC	AAT	CCT	TCT	GTT	TCT	5940
1966	G	E	G	N	V	D	E	T	G	N	N	P	S	V	S	1980
5941	TTA	AAA	CTG	GAA	GAA	AGT	AAA	GCT	ACT	TCT	TCT	TCT	AAT	CCA	AGC	5985
1981	L	K	L	E	E	S	K	A	T	S	S	S	N	P	S	1995
5986	AGC	CCA	GCT	CCA	GAC	TGG	TAC	AAA	GAT	TTT	GTT	ACA	GAT	GCT	GAT	6030
1996	S	P	A	P	D	W	Y	K	D	F	V	T	D	A	D	2010
6031	GCT	GAG	GTT	TTA	GAG	CAT	TCT	GGG	AAA	ATG	GTA	CTT	CTC	TTT	GAA	6075
2011	A	E	V	L	E	H	S	G	K	M	V	L	L	F	E	2025
6076	ATT	CTT	CGA	ATG	GCA	GAG	GAA	ATT	GGG	GAT	AAA	GTC	CTT	GTT	TTC	6120
2026	I	L	R	M	A	E	E	I	G	D	K	V	L	V	F	2040
6121	AGC	CAG	TCC	CTC	ATA	TCT	CTG	GAC	TTG	ATT	GAA	GAT	TTT	CTT	GAA	6165
2041	S	Q	S	L	I	S	L	D	L	I	E	D	F	L	E	2055
6166	TTA	GCT	AGT	AGG	GAG	AAG	ACA	GAA	GAT	AAA	GAT	AAA	CCC	CTT	ATT	6210
2056	L	A	S	R	E	K	T	E	D	K	D	K	P	L	I	2070
6211	TAT	AAA	GGT	GAG	GGG	AAG	TGG	CTT	CGA	AAC	ATT	GAC	TAT	TAC	CGT	6255
2071	Y	K	G	E	G	K	W	L	R	N	I	D	Y	Y	R	2085
6256	TTA	GAT	GGT	TCC	ACT	ACT	GCA	CAG	TCA	AGG	AAG	AAG	TGG	GCT	GAA	6300
2086	L	D	G	S	T	T	A	Q	S	R	K	K	W	A	E	2100
6301	GAA	TTT	AAT	GAT	GAA	ACT	AAT	GTG	AGA	GGA	CGA	TTA	TTT	ATC	ATT	6345
2101	E	F	N	D	E	T	N	V	R	G	R	L	F	I	I	2115
6346	TCT	ACT	AAA	GCA	GGA	TCT	CTA	GGA	ATT	AAT	CTG	GTA	GCT	GCT	AAT	6390
2116	S	T	K	A	G	S	L	G	I	N	L	V	A	A	N	2130
6391	CGA	GTA	ATT	ATA	TTC	GAC	GCT	TCT	TGG	AAT	CCA	TCT	TAT	GAC	ATC	6435
2131	R	V	I	I	F	D	A	S	W	N	P	S	Y	D	I	2145
6436	CAG	AGT	ATA	TTC	AGA	GTT	TAT	CGC	TTT	GGA	CAA	ACT	AAG	CCT	GTT	6480
2146	Q	S	I	F	R	V	Y	R	F	G	Q	T	K	P	V	2160
6481	TAT	GTA	TAT	AGG	TTC	TTA	GCT	CAG	GGA	ACC	ATG	GAA	GAT	AAG	ATT	6525
2161	Y	V	Y	R	F	L	A	Q	G	T	M	E	D	K	I	2175
6526	TAT	GAT	CGG	CAA	GTA	ACT	AAG	CAG	TCA	CTG	TCT	TTT	CGA	GTT	GTT	6570
2176	Y	D	R	Q	V	T	K	Q	S	L	S	F	R	V	V	2190
6571	GAT	CAG	CAG	CAG	GTG	GAG	CGT	CAT	TTT	ACT	ATG	AAT	GAG	CTT	ACT	6615
2191	D	Q	Q	Q	V	E	R	H	F	T	M	N	E	L	T	2205
6616	GAA	CTT	TAT	ACT	TTT	GAG	CCA	GAC	TTA	TTA	GAT	GAC	CCT	AAT	TCA	6660
2206	E	L	Y	T	F	E	P	D	L	L	D	D	P	N	S	2220
6661	GAA	AAG	AAG	AAG	AAG	AGG	GAT	ACT	CCC	ATG	CTG	CCA	AAG	GAT	ACC	6705
2221	E	K	K	K	K	R	D	T	P	M	L	P	K	D	T	2235
6706	ATA	CTT	GCA	GAG	CTC	CTT	CAG	ATA	CAT	AAA	GAA	CAC	ATT	GTA	GGA	6750

2236	I	L	A	E	L	L	Q	I	H	K	E	H	I	V	G	2250
6751	TAC	CAT	GAA	CAT	GAT	TCT	CTT	TTG	GAC	CAC	AAA	GAA	GAA	GAA	GAG	6795
2251	Y	H	E	H	D	S	L	L	D	H	K	E	E	E	E	2265
6796	TTG	ACT	GAA	GAA	GAA	AGA	AAA	GCA	GCT	TGG	GCT	GAG	TAT	GAA	GCA	6840
2266	L	T	E	E	E	R	K	A	A	W	A	E	Y	E	A	2280
6841	GAG	AAG	AAG	GTA	CTG	ACC	ATG	CGT	TTC	AAC	ATA	CCA	ACT	GGG	ACC	6885
2281	E	K	K	V	L	T	M	R	F	N	I	P	T	G	T	2295
6886	AAT	TTA	CCC	CCT	GTC	AGT	TTC	AAC	TCT	CAA	ACT	CCT	TAT	ATT	CCT	6930
2296	N	L	P	P	V	S	F	N	S	Q	T	P	Y	I	P	2310
6931	TTC	AAT	TTG	GGA	GCC	CTG	TCA	GCA	ATG	AGT	AAT	CAA	CAG	CTG	GAG	6975
2311	F	N	L	G	A	L	S	A	M	S	N	Q	Q	L	E	2325
6976	GAC	CTC	ATT	AAT	CAA	GGA	AGA	GAA	AAA	GTT	GTA	GAA	GCA	ACA	AAC	7020
2326	D	L	I	N	Q	G	R	E	K	V	V	E	A	T	N	2340
7021	AGT	GTG	ACA	GCA	GTG	AGG	ATT	CAA	CCT	CTT	GAG	GAT	ATA	ATT	TCA	7065
2341	S	V	T	A	V	R	I	Q	P	L	E	D	I	I	S	2355
7066	GCT	GTA	TGG	AAG	GAG	AAC	ATG	AAT	CTC	TCA	GAG	GCC	CAA	GTA	CAG	7110
2356	A	V	W	K	E	N	M	N	L	S	E	A	Q	V	Q	2370
7111	GCG	TTA	GCA	TTA	AGT	AGA	CAA	GCC	AGC	CAG	GAG	CTT	GAT	GTT	AAA	7155
2371	A	L	A	L	S	R	Q	A	S	Q	E	L	D	V	K	2385
7156	CGA	AGA	GAA	GCA	ATC	TAC	AAT	GAT	GTA	TTG	ACA	AAA	CAA	CAG	ATG	7200
2386	R	R	E	A	I	Y	N	D	V	L	T	K	Q	Q	M	2400
7201	TTA	ATC	AGC	TGT	GTT	CAG	CGA	ATA	CTT	ATG	AAC	AGA	AGG	CTC	CAG	7245
2401	L	I	S	C	V	Q	R	I	L	M	N	R	R	L	Q	2415
7246	CAG	CAG	TAC	AAT	CAG	CAG	CAA	CAG	CAA	CAA	ATG	ACT	TAT	CAA	CAA	7290
2416	Q	Q	Y	N	Q	Q	Q	Q	Q	Q	M	T	Y	Q	Q	2430
7291	GCA	ACA	CTG	GGT	CAC	CTC	ATG	ATG	CCA	AAG	CCC	CCA	AAT	TTG	ATC	7335
2431	A	T	L	G	H	L	M	M	P	K	P	P	N	L	I	2445
7336	ATG	AAT	CCT	TCT	AAC	TAC	CAG	CAG	ATT	GAT	ATG	AGA	GGA	ATG	TAT	7380
2446	M	N	P	S	N	Y	Q	Q	I	D	M	R	G	M	Y	2460
7381	CAG	CCA	GTG	GCT	GGT	GGT	ATG	CAG	CCA	CCA	CCA	TTA	CAG	CGT	GCA	7425
2461	Q	P	V	A	G	G	M	Q	P	P	P	L	Q	R	A	2475
7426	CCA	CCC	CCA	ATG	AGA	AGC	AAA	AAT	CCA	GGA	CCT	TCC	CAA	GGG	AAA	7470
2476	P	P	P	M	R	S	K	N	P	G	P	S	Q	G	K	2490
7471	TCA	ATG	TGA													7479
2491	S	M	*													

Figure 2:
ATRX Antisense fragments

Fragment No. 1: HAP_66D4 (SEQ ID NO:3)

5' TGCACCTGCCTTTCCTCTTCCACCTTCACTATTATTGCCCACACCTGTTAAGTGATCTAAGT
AGTACTGATAGAGCTTGCACCTGAATAGAAGTCATTCTCACAGCTAACACATATTCGTGTTTTGG
AGGCAAGAATTTTGTTAATGCTGTATAATCTTTCCTCTGAACACATCCAGCTAACATCTCATAG
AGAATGTGAGCACGTTTTTTCATCACTCTGACATCTACCATGGTAGAATCTGCACACTGACCAT
TTTGAATTGGATTATATAAATCTATTCCTGAACTCCTTAAT 3'

Fragment No. 2: TXA_1B3 (SEQ ID NO:4)

5' GCTTTAGTGCAAATACATTGATTTCCCTTGGGAAGGTCCTGGATTTTTGCTTCTCATTGGGG
GTGGTGCACGCTGTAATGGTGGTGGCTGCATACCACCAGCCACTGGCTGATACATTCCTCTCAT
ATCAATCTGCTGGTAGTTAGAAGGATTCATGATCAAATTTGGGGGCTTTGGCATCATGAGGTGA
CCCAGTGTTGCTTGTTGATAAGTCATTTGTTGCTGTTGCTGCTGATTGTACTGCTGCTGGAGCC
TTCTGTTTCATAAGTATTCGCTGAACACAGCTGATTAACATCT 3'

Figure 3:
Alignment between the ATRX open reading frame and the corresponding sense polynucleotide of the ATRX Antisense Fragments

a) AS Fragment No. 1 (HAP-66D4)

ATRX ORF	1	ATGACCGCTGAGCCCATGAGTGAAAGCAAGTTGAATACATTGGTGCAGAAGCTTCATGACTTCCTTGACACTCATCAGA
HAP-66D4	1	-----
ATRX ORF	81	AGAATCTGAAGAAACAAGTTCTCTCCACGACTTGCAATGAATCAAAACACAGATAAAATCAGTGGTTCTGGAAGTAACT
HAP-66D4	1	-----
ATRX ORF	161	CTGATATGATGGAAAACAGCAAGGAAGAGGGAAGTACTCTTCAGAAAAATCCAAGTCTTCAGGATCGTCACGATCAAAG
HAP-66D4	1	-----
ATRX ORF	241	AGGAAACCTTCAATTGTAAACAAAGTATGTAGAATCAGATGATGAAAAACCTTTGGATGATGAAACTGTAAATGAAGATGC
HAP-66D4	1	-----
ATRX ORF	321	GTCTAATGAAAATTCAGAAAATGATATTACTATGCAGAGCTTGCCAAAAGGTACAGTGATTGTACAGCCAGAGCCAGTGC
HAP-66D4	1	-----
ATRX ORF	401	TGAATGAAGACAAAGATGATTTTAAAGGGCCTGAATTTAGAAGCAGAAGTAAATGAAAACCTGAAAATCTCAAAAAACGC
HAP-66D4	1	-----
ATRX ORF	481	GGAGAAGATGGGCTTCATGGGATTGTGAGCTGCACTGCTTGTGGACAACAGGTCAATCATTTTCAAAAAGATTCCATTTA
HAP-66D4	1	-----
ATRX ORF	561	TAGACACCTTCATTGCAAGTTCTTATTGTAAAGATTGCTTTAAGTATTACATGAGTGATGATATTAGCCGTGACTCAG
HAP-66D4	1	-----
ATRX ORF	641	ATGGAATGGATGAACAATGTAGGTGGTGTGCGGAAGGTGGAAACTTGATTGTGTGACTTTTGCCATAATGCTTTCTGTC
HAP-66D4	1	-----
ATRX ORF	721	AAGAAATGCATTCTACGCAACCTTGGTCGAAAGGAGTTGTCCACAATAATGGATGAAAACAACCAATGGTATTGCTACAT
HAP-66D4	1	-----
ATRX ORF	801	TTGTCACCCAGAGCCTTTGTTGGACTTGGTCACTGCATGTAACAGCGTATTTGAGAATTTAGAACAGTTGTTGCAGCAAA
HAP-66D4	1	-----
ATRX ORF	881	ATAAGAAGAAGATAAAAGTTGACAGTGAAAAGAGTAATAAGTATATGAACATACATCCAGATTTTCTCCAAAGAAGACT
HAP-66D4	1	-----
ATRX ORF	961	AGTTCAAATTGTAATGGAGAAGAAAAGAAATTAGATGATTCTGTCTGGCTCTGTAACCTACTCTTATTCCGCACTAAT
HAP-66D4	1	-----
ATRX ORF	1041	TGTGCCCAAGAGATGATTAAGAAGGCAAAAAAAGTATTGAGACCACAGCCAACATGAACTCCAGTTATGTTAAATTTT
HAP-66D4	1	-----
ATRX ORF	1121	TAAAGCAGGCAACAGATAATTCAGAAATCAGTTCTGCTACAAAATTACGTCAGCTTAAGGCTTTTAAGTCTGTGTTGGCT
HAP-66D4	1	-----
ATRX ORF	1201	GATATTAAGAAGGCTCATCTTGCAATTGGAAGAAGACTTAATTCGAGTTTCGAGCGATGGATGCTGTAACAAAGAGAA
HAP-66D4	1	-----
ATRX ORF	1281	AAATACCAAGAGCATAAAGTCATAGATGCTAAGTTTGAACAAAAGCACGAAAAGGAGAAAAACCTTGTGCTTTGGAAA
HAP-66D4	1	-----
ATRX ORF	1361	AGAAGGATATTTCAAAGTCAGAAAGCTAACTTTCAAGAAAACAGGTAGATAGTGAGCACATGCATCAGAATGTTCCAACA
HAP-66D4	1	-----
ATRX ORF	1441	GAGGAACAAGAACAAATAAAAGYACCGGTGGTGAACATAAGAAATCTGATAGAAAAGAAGAACCTCAATATGAACCTGC
HAP-66D4	1	-----
ATRX ORF	1521	CAACACTTCTGAAGATTTAGACATGGATATTGTGTCTGTTCCCTCCTCAGTTCCAGAAGACATTTTGTGAGATCTTGAGA
HAP-66D4	1	-----
ATRX ORF	1601	CTGCTATGGAAGTTCAGAGTTCAGTTGATCATCAAGGGGATGGCAGCAGTGGAACTGAACAAGAAGTGGAGAGTTTCATCT
HAP-66D4	1	-----
ATRX ORF	1681	GTAAAATTAAATATTTCTTCAAAAGACAACAGAGGAGGTATTAAATCAAAAACCTACAGCTAAAGTAACAAAAGAATTATA

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HAP-66D4 1 -----
ATRX ORF 1761 TGTTAAACTCACTCTGTTTCCCTTCCTAATCCCAATTAAAGGTGCTGATTGTCAGGAAGTTCCACAAGATAAAGATG
HAP-66D4 1 -----
ATRX ORF 1841 GCTATAAAAGTTGTGGTCTGAACCCCAAGTTAGAGAAATGTGGACTTGGACAGGAAAACAGTGATAATGAGCATTGGTT
HAP-66D4 1 -----
ATRX ORF 1921 GAAATGAAGTTTCATTACTTTTAGAGGAATCTGATCTTCGGAGATCCCCACGTGTAAGACTACACCCTTGAGGCGACC
HAP-66D4 1 -----
ATRX ORF 2001 GACAGAACTAACCTGTAACATCTAATTCAGATGAAGAATGTAAAGAAACAGTTAAGGAGAAACAAAACTATCAGTTC
HAP-66D4 1 -----
ATRX ORF 2081 CAGTGAGAAAAAGGATAAGCGTAATCTTCTGACAGTGTATAGATAATCCTAAGCCTAATAAATTGCCAAATCTAAG
HAP-66D4 1 -----
ATRX ORF 2161 CAATCAGAGACTGTGGATCAAATTCAGATTCTGATGAAATGCTAGCAATCCTCAAAGGGGTGAGCAGGATGAGTCACAG
HAP-66D4 1 -----
ATRX ORF 2241 TTCTTCTCAGATACTGATATTAATGAAATTCATACAAACCATAAGACTTTGTATGATTTAAAGACTCAGGCGGGGAAAG
HAP-66D4 1 -----
ATRX ORF 2321 ATGATAAAGGAAAAAGGAAACGAAAAAGTTCTACATCTGGCTCAGATTTTGATACTAAAAAGGGCAAATCAGCTAAGAGC
HAP-66D4 1 -----
ATRX ORF 2401 TCTATAATTTCTAAAAAGAACGACAAACCCAGTCTGAGTCTTCTAATTATGACTCAGAATTAGAAAAAGAGATAAAGAG
HAP-66D4 1 -----
ATRX ORF 2481 CATGAGTAAATTTGGTGCTGCCAGAACCCAAAAAAGAATTCCAATACAAAAGATTTTGACTCTTCTGAAGATGAGA
HAP-66D4 1 -----
ATRX ORF 2561 AACACAGCAAAAAAGGAATGGATAATCAAGGGCACAAAAATTTGAAGACCTCACAAGAAGGATCATCTGATGATGCTGAA
HAP-66D4 1 -----
ATRX ORF 2641 AGAAAAACAAGAGAGAGAGACTTTCTCTTCAGCAGAAGGCACAGTTGATAAAGACACGACCATCATGGAATTAAGAGATCG
HAP-66D4 1 -----
ATRX ORF 2721 ACTTCCTAAGAAGCAGCAAGCAAGTGCTTCCACTGATGGTGTCGATAAGCTTTCTGGGAAAGAGCAGAGTTTACTTCTT
HAP-66D4 1 -----
ATRX ORF 2801 TGGAAGTTAGAAAAGTTGCTGAACTAAAGAAAAGAGCAAGCATCTCAAAACCAAACATGTAAAAAGTACAGGATGGC
HAP-66D4 1 -----
ATRX ORF 2881 TTATCTGATATTGCAGAGAAATTCCTAAAGAAAGACCAGAGCGATGAACTTCTGAAGATGATAAAAGCAGAGCAAAAA
HAP-66D4 1 -----
ATRX ORF 2961 GGGAACTGAAGAAAAAAGAAACCTTCAGACTTTAAGAAAAAGTAATTAATGGAACAACAGTATGAATCTTCATCTG
HAP-66D4 1 -----
ATRX ORF 3041 ATGGCACTGAAAAGTTACCTGAGCGAGAAGAAATTTGTCATTTTCTAAGGGCATAAACAAATTAAGAATGGAACAAC
HAP-66D4 1 -----
ATRX ORF 3121 GATGGAGAAAAGAAAAGTAAAAAATAAGAGATAAACTTCTAAAAAGAGGATGAATTATCTGATTATGCTGAGAAGTC
HAP-66D4 1 -----
ATRX ORF 3201 AACAGGGAAGGAGATAGTTGTGACTCTTCAGAGGATAAAAGAGTAAGAATGGAGCATATGGTAGAGAGAAGAAAAGGT
HAP-66D4 1 -----
ATRX ORF 3281 GCAAGTTGCTTGGAAGAGTTCAAGGAAGAGACAAGATTGCTCATCTGATACTGAGAAATATTCATGAAAGAAGAT
HAP-66D4 1 -----
ATRX ORF 3361 GGTTGTAACCTTCTGATAAGAGACTGAAAAGAATAGAATTGAGGGAAAGAAGAAATTTAAGTTCAAAGAGAAATACTAA
HAP-66D4 1 -----
ATRX ORF 3441 GGAAATACAAAGTGGCTCATCATCTGATGCTGAGGAAAGTTCTGAAGATAATAAAAGAAGAAGCAAAGAACCTTCAT
HAP-66D4 1 -----
ATRX ORF 3521 CTAAAAAGAAGGCAGTCATTGTCAAGGAGAAAAAGAGAACTCCCTAAGAACAAGCACTAAAAGGAAGCAAGCTGACATT
HAP-66D4 1 -----
ATRX ORF 3601 ACATCCTCATCTTCTTCTGATATAGAAGATGATGATCAGAATTCTATAGGTGAGGGAAGCAGCGATGAACAGAAAATTAA
HAP-66D4 1 -----

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ATRX ORF 3681 GCCTGTCACTGAAAATTTAGTGTCTTTCACATACTGGATTTTGCCAATCTTCAGGAGATGAAGCCTTATCTAAATCAG
 HAP-66D4 1 -----
 ATRX ORF 3761 TGCCTGTCACAGTGGATGATGATGATGACGACAATGATCCTGAGAATAGAATTGCCAAGAAGATGCTTTTAGAAGAAATT
 HAP-66D4 1 -----
 ATRX ORF 3841 AAAGCCAATCTTCTCTGATGAGGATGGATCTTCAGATGATGAGCCAGAAGAAGGGAAAAAAGAACTGGAAAACAAAA
 HAP-66D4 1 -----
 ATRX ORF 3921 TGAAGAAAACCCAGGAGATGAGGAAGCAAAAAATCAAGTCAATTCTGAATCAGATTCAGATTCTGAAGAATCTAAGAAGC
 HAP-66D4 1 -----
 ATRX ORF 4001 CAAGATACAGACATAGGCTTTTGC GGCACAAATTGACTGTGAGTGACGGAGAATCTGGAGAAGAAAAAAGACAAAGCCT
 HAP-66D4 1 -----
 ATRX ORF 4081 AAAGAGCATAAAGAAGTCAAAGGCAGAAACAGAAGAAAGGTGAGCAGTGAAGATTCAGAAGATTCTGATTTTCAGGAATC
 HAP-66D4 1 -----
 ATRX ORF 4161 AGGAGTTAGTGAAGAAGTTAGTGAATCCGAAGATGAACAGCGGCCCAGAACAAGGTCTGCAAGAAAGCAGAGTTGGAAG
 HAP-66D4 1 -----
 ATRX ORF 4241 AAAATCAGCGGAGCTATAAACAGAAAAAGAAAAGGCGACGTATTAAGGTTCAAGAAGATTCTCCAGTGAAAACAAGAGT
 HAP-66D4 1 -----
 ATRX ORF 4321 AATTCTGAGGAAGAAGAGGAGGAAAAAGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAAGATGAAAA
 HAP-66D4 1 -----
 ATRX ORF 4401 TGATGATTCCAAGTCTCCTGGAAAAGGCAGAAAGAAAATTTCGGAAGATTCTTAAGATGATAAACTGAGAACAGAAACAC
 HAP-66D4 1 -----
 ATRX ORF 4481 AAAATGCTCTTAAGGAAGAGGAAGAGAGACGAAACGTATTGCTGAGAGGGAGCGTGAGCGAGAAAAATTGAGAGAGGTG
 HAP-66D4 1 -----
 ATRX ORF 4561 ATAGAAATTGAAGATGCTTCACCCACCAAGTGTCGAATAACAACCAAGTTGGTTTTAGATGAAGATGAAGAAACCAAAGA
 HAP-66D4 1 -----
 ATRX ORF 4641 ACCTTTAGTGCAGGTTTCATAGAAATATGGTTATCAAATTGAAACCCCATCAAGTAGATGGTGTTTATGTGGGATT
 HAP-66D4 1 -----
 ATRX ORF 4721 GCTGCTGTGAGTCTGTGAAAAAACAAAGAAATCTCCAGGTTTCAGGATGCATTCTTGCCCACTGTATGGGCCTTGGTAAG
 HAP-66D4 1 -----
 ATRX ORF 4801 ACTTTACAGGTGGTAAGTTTCTTCATACAGTTCTTTTGTGTGACAAACTGGATTTTCAGCACGGCGTTAGTGGTTTGTCC
 HAP-66D4 1 -----
 ATRX ORF 4881 TCTTAATACTGCTTTGAATTGGATGAATGAATTGAGAAGTGGCAAGAGGGATTAAAAGATGATGAGAAGCTTGAGGTTT
 HAP-66D4 1 -----
 ATRX ORF 4961 CTGAATTAGCAACTGTGAAACGTCCTCAGGAGAGAAGCTACATGCTGCAGAGGTGGCAAGAAGATGGTGGTGTTATGATC
 HAP-66D4 1 -----
 ATRX ORF 5041 ATAGGCTATGAGATGTATAGAAATCTTGCTCAAGGAAGGAATGTGAAGAGTCGGAACTTAAAGAAATATTTAACAAAGC
 HAP-66D4 1 -----
 ATRX ORF 5121 TTTGGTTGATCCAGGCCCTGATTTTGTGTTTGTGATGAAGGCCATATTCTAAAAATGAAGCATCTGCTGTTTCTAAAG
 HAP-66D4 1 -----
 ATRX ORF 5201 CTATGAATTCATACGATCAAGGAGGAGGATTATTTTAACAGGAACACCACTTCAAATAACCTAATTGAGTATCATTGT
 HAP-66D4 1 -----
 ATRX ORF 5281 ATGGTTAATTTTATCAAGGAAAAATTTACTTGGATCCATTAAAGGAGTTCAGGAATAGATTATATAATCCAATTCAAAATGG
 HAP-66D4 1 -----ATTAAAGGAGTTCAGGAATAGATTATATAATCCAATTCAAAATGG
 ATRX ORF 5361 TCAGTGTGCAGATTCTACCATGGTAGATGTCAAGTGTGAAAAACGTCCTCACATTCTCTATGAGATGTTAGCTGGAT
 HAP-66D4 45 TCAGTGTGCAGATTCTACCATGGTAGATGTCAAGTGTGAAAAACGTCCTCACATTCTCTATGAGATGTTAGCTGGAT
 ATRX ORF 5441 GTGTTTCAGAGGAAGATTATACAGCATTAAACAAAATTTCTTGCCCTCCAAAACACGAATATGTGTTAGCTGTGAGAATGACT
 HAP-66D4 125 GTGTTTCAGAGGAAGATTATACAGCATTAAACAAAATTTCTTGCCCTCCAAAACACGAATATGTGTTAGCTGTGAGAATGACT
 ATRX ORF 5521 TCTATTTCAGTGCAGCTCTATCAGTACTACTTAGATCACTTAACAGGTGTGGGCAATAATAGTGAAGCTGGAAGAGGAAA
 HAP-66D4 205 TCTATTTCAGTGCAGCTCTATCAGTACTACTTAGATCACTTAACAGGTGTGGGCAATAATAGTGAAGCTGGAAGAGGAAA

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ATRX ORF 5601 GGCAGGTGCAAGCTTTTCCAAGATTTTCAGATGTTAAGTAGAATATGGACTCATCCTTGGTGTTCAGCTAGACTACA
HAP-66D4 285 GGCAGGTGCA-----
ATRX ORF 5681 TTAGCAAAGAAAATAAGGGTTATTTTGATGAAGACAGTATGGATGAATTTATAGCCTCAGATTCTGATGAAACCTCCATG
HAP-66D4 294 -----
ATRX ORF 5761 AGTTTAAGCTCCGATGATTATACAAAAAGAAGAAAAAGGGAAAAAGGGAAAAAGATAGTAGCTCAAGTGGAAGTGG
HAP-66D4 294 -----
ATRX ORF 5841 CAGTGACAATGATGTTGAAGTGATTAAGGTCTGGAATTCAGATCTCGGGGAGGTGGTGAAGGAAATGTGGATGAAACAG
HAP-66D4 294 -----
ATRX ORF 5921 GAAACAATCCTTCTGTTTCTTTAAACTGGAAGAAAGTAAAGCTACTTCTTCTTAATCCAAGCAGCCCAGCTCCAGAC
HAP-66D4 294 -----
ATRX ORF 6001 TGGTACAAAGATTTTGTTACAGATGCTGATGCTGAGGTTTAGAGCATTCTGGGAAATGGTACTTCTCTTGAAATTCT
HAP-66D4 294 -----
ATRX ORF 6081 TCGAATGGCAGAGGAAATGGGGATAAAGTCCTTGTTTTCAGCCAGTCCCTCATATCTCTGGACTTGATTGAAGATTTTC
HAP-66D4 294 -----
ATRX ORF 6161 TTGAATTAGCTAGTAGGGAGAAGACAGAAGATAAAGATAAACCCCTTATTTATAAAGGTGAGGGGAAGTGGCTTCGAAAC
HAP-66D4 294 -----
ATRX ORF 6241 ATTGACTATTACCGTTTAGATGGTTCCACTACTGCACAGTCAAGGAAGAAGTGGGCTGAAGAATTTAATGATGAACTAA
HAP-66D4 294 -----
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HAP-66D4 294 -----
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ATRX ORF 6801 TGAAGAAGAAAGAAAGCAGCTTGGGCTGAGTATGAAGCAGAGAAGAAGTACTGACCATGCGTTTCAACATACCAACTG
HAP-66D4 294 -----
ATRX ORF 6881 GGACCAATTTACCCCTGTGAGTTTCAACTCTCAAACCTCCTTATATTCCTTTCAATTTGGGAGCCCTGTGAGCAATGAGT
HAP-66D4 294 -----
ATRX ORF 6961 AATCAACAGCTGGAGGACCTCATTAATCAAGGAAGAGAAAAAGTTGAGAAGCAACAACAGTGTGACAGCAGTGAGGAT
HAP-66D4 294 -----
ATRX ORF 7041 TCAACCTCTTGAGGATATAATTTAGCTGTATGGAAGGAGAACATGAATCTCTCAGAGGCCCAAGTACAGGCGTTAGCAT
HAP-66D4 294 -----
ATRX ORF 7121 TAAGTAGACAAGCCAGCCAGGAGCTTGATGTTAAACGAAGAGAAGCAATCTACAATGATGTATTGACAAAACAACAGATG
HAP-66D4 294 -----
ATRX ORF 7201 TTAATCAGCTGTGTTGAGCGAATACTTATGAACAGAAGGCTCCAGCAGCAGTACAATCAGCAGCAACAGCAACAAATGAC
HAP-66D4 294 -----
ATRX ORF 7281 TTATCAACAAGCAACACTGGGTACCTCATGATGCCAAAGCCCCCAAATTTGATCATGAATCCTTCTAACTACCAGCAGA
HAP-66D4 294 -----
ATRX ORF 7361 TTGATATGAGAGGAATGTATCAGCCAGTGGCTGGTGGTATGCAGCCACCACCATTACAGCGTGACCAACCCCAATGAGA
HAP-66D4 294 -----
ATRX ORF 7441 AGCAAAAATCCAGGACCTTCCCAAGGGAAATCAATGTGA
HAP-66D4 294 -----

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b) AS fragm nt No. 2 (TXA-1B3)

ATRX ORF	1	ATGACCGCTGAGCCCATGAGTGAAAGCAAGTTGAATACATTGGTGCAGAAGCTTCATGACTTCCTTGCACACTCATCAGA
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ATRX ORF	81	AGAATCTGAAGAAACAAGTTCTCTCCACGACTTGCAATGAATCAAAACACAGATAAAATCAGTGGTTCTGGAAGTAACT
TXA-1B3	1	-----
ATRX ORF	161	CTGATATGATGGAACAGCAAGGAAGAGGGAAGTACTAGTCTTCAGAAAAATCCAAGTCTTCAGGATCGTCACGATCAAAG
TXA-1B3	1	-----
ATRX ORF	241	AGGAAACCTTCAATTGTAACAAAGTATGTAGAATCAGATGATGAAAAACCTTTGGATGATGAAACTGTAAATGAAGATGC
TXA-1B3	1	-----
ATRX ORF	321	GTCTAATGAAATTCAGAAAAATGATATTACTATGCAGAGCTTGCCAAAAGGTACAGTGATTGTACAGCCAGAGCCAGTGC
TXA-1B3	1	-----
ATRX ORF	401	TGAATGAAGACAAAGATGATTTTAAAGGGCCTGAATTTAGAAGCAGAAGTAAATGAAACTGAAAATCTCAAAAAACGC
TXA-1B3	1	-----
ATRX ORF	481	GGAGAAGATGGGCTTCATGGGATTGTGAGCTGCACTGCTTGTGGACAACAGGTCAATCATTTTTCAAAAAGATTCCATTTA
TXA-1B3	1	-----
ATRX ORF	561	TAGACACCTTCATTCGAAGTCTTATTTGTAAGAATTGCTTTAAGTATTACATGAGTGATGATATTAGCCGTGACTCAG
TXA-1B3	1	-----
ATRX ORF	641	ATGGAATGGATGAACAATGTAGGTGGTGTGCGGAAGGTGGAACCTTGATTTGTTGTGACTTTTGCCATAATGCTTTCTGC
TXA-1B3	1	-----
ATRX ORF	721	AAGAAATGCATTCTACGCAACCTTGGTCGAAAGGAGTTGTCCACAATAATGGATGAAAACAACCAATGGTATTGCTACAT
TXA-1B3	1	-----
ATRX ORF	801	TTGTCACCCAGAGCCTTTGTGGACTTGGTCACTGCATGTAACAGCGTATTTGAGAATTTAGAACAGTTGTTGCAGCAAA
TXA-1B3	1	-----
ATRX ORF	881	ATAAGAAGAAGATAAAAGTTGACAGTGAAAAGAGTAATAAAGTATATGAACATACATCCAGATTTTCTCCAAAGAAGACT
TXA-1B3	1	-----
ATRX ORF	961	AGTTCAAATTGTAATGGAGAAGAAAAGAAATTAGATGATTCCTGTTCTGGCTCTGTAACCTACTCTTATTCGCACTAAT
TXA-1B3	1	-----
ATRX ORF	1041	TGTGCCCCAAGAGATGATTAAGAAGGCCAAAAAACTGATTGAGACCACAGCCAACATGAACTCCAGTTATGTTAAATTTT
TXA-1B3	1	-----
ATRX ORF	1121	TAAAGCAGGCAACAGATAATTCAGAAATCAGTTCTGCTACAAAATTACGTCAGCTTAAGGCTTTTAAGTCTGTGTTGGCT
TXA-1B3	1	-----
ATRX ORF	1201	GATATTAAGAAGGCTCATCTTGCATTGGAAGAAGACTTAAATTCCGAGTTTCGAGCGATGGATGCTGTAAACAAAGAGAA
TXA-1B3	1	-----
ATRX ORF	1281	AAATACCAAGAGCATAAAGTCATAGATGCTAAGTTTGAACAAAAGCACGAAAAGGAGAAAAACCTTGTGCTTTGGAAA
TXA-1B3	1	-----
ATRX ORF	1361	AGAAGGATATTTCAAAGTCAGAAGCTAACTTTCAAGAAAACAGGTAGATAGTGAGCACATGCATCAGAATGTTCCAACA
TXA-1B3	1	-----
ATRX ORF	1441	GAGGAACAAAGAACAATAAAAGYACCGGTGGTGAACATAAGAAATCTGATAGAAAAGAAGAACCTCAATATGAACCTGC
TXA-1B3	1	-----
ATRX ORF	1521	CAACACTTCTGAAGATTTAGACATGGATATTGTGCTGTTCCCTTCCTCAGTTCCAGAAGACATTTTTGAGAATCTTGAGA
TXA-1B3	1	-----
ATRX ORF	1601	CTGCTATGGAAGTTCAGAGTTCAGTTGATCATCAAGGGGATGGCAGCAGTGGAACTGAACAAGAAGTGGAGAGTTTCATCT
TXA-1B3	1	-----
ATRX ORF	1681	GTAAATTAATATTTCTTCAAAGACAACAGAGGAGGTATTAATCAAAAACCTACAGCTAAAGTAACAAAAGAATTATA
TXA-1B3	1	-----
ATRX ORF	1761	TGTTAAACTCACTCCTGTTTCCCTTCCATAATCCCAATTAAGGTGCTGATTGTCAGGAAGTTCCACAAGATAAAGATG

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TXA-1B3 1 -----
ATRX ORF 1841 GCTATAAAAGTTGTGGTCTGAACCCCAAGTTAGAGAAATGTGGACTTGGACAGGAAAACAGTGATAATGAGCATTGTT
TXA-1B3 1 -----
ATRX ORF 1921 GAAAAAGAAGTTTCATTACTTTTAGAGGAATCTGATCTTCGGAGATCCCCACGTGTAAGACTACACCCTTGAGGCGACC
TXA-1B3 1 -----
ATRX ORF 2001 GACAGAACTAACCTGTAACATCTAATTCAGATGAAGAATGTAATGAAACAGTTAAGGAGAAACAAAACTATCAGTTC
TXA-1B3 1 -----
ATRX ORF 2081 CAGTGAGAAAAAGGATAAGCGTAATTCTTCTGACAGTGCTATAGATAATCCTAAGCCTAATAAATTGCCAAAATCTAAG
TXA-1B3 1 -----
ATRX ORF 2161 CAATCAGAGACTGTGGATCAAAATTCAGATTCTGATGAAATGCTAGCAATCCTCAAAGGGTGAGCAGGATGAGTCACAG
TXA-1B3 1 -----
ATRX ORF 2241 TTCTTCTTCAGATACTGATATTAATGAAATTACATAAACCATAGACTTTGTATGATTTAAAGACTCAGCGGGGAAAG
TXA-1B3 1 -----
ATRX ORF 2321 ATGATAAAGGAAAAGGAAACGAAAAAGTTCTACATCTGGCTCAGATTTTGATACTAAAAGGGCAAATCAGCTAAGAGC
TXA-1B3 1 -----
ATRX ORF 2401 TCTATAATTTCTAAAAGAAACGACAAACCCAGTCTGAGTCTTCTAATTATGACTCAGAATTAGAAAAGAGATAAAGAG
TXA-1B3 1 -----
ATRX ORF 2481 CATGAGTAAATTTGGTGCTGCCAGAACCACCAAAAAAGAATTCCAATACAAAAGATTTTGACTCTTCTGAAGATGAGA
TXA-1B3 1 -----
ATRX ORF 2561 AACACAGCAAAAAAGGAATGGATAATCAAGGGCACAAAAATTTGAAGACCTCACAAGAAGGATCATCTGATGATGCTGAA
TXA-1B3 1 -----
ATRX ORF 2641 AGAAAACAAGAGAGAGAGACTTTCTCTTCAGCAGAAGGCACAGTTGATAAAGACACGACCATCATGGAATTAAGAGATCG
TXA-1B3 1 -----
ATRX ORF 2721 ACTTCCTAAGAAGCAGCAAGCAAGTGCTTCCACTGATGGTGTGATAAGCTTTCTGGGAAAGAGCAGAGTTTACTTCTT
TXA-1B3 1 -----
ATRX ORF 2801 TGGAAGTTAGAAAAGTTGCTGAAACTAAAGAAAAGAGCAAGCATCTCAAACCAAACATGTAAAAAGTACAGGATGGC
TXA-1B3 1 -----
ATRX ORF 2881 TTATCTGATATTGCAGAGAAATTCCTAAAGAAAGACCAGAGCGATGAACTTCTGAAGATGATAAAAGCAGAGCAAAAA
TXA-1B3 1 -----
ATRX ORF 2961 GGGAACTGAAGAAAAAAGAAACCTTCAGACTTTAAGAAAAAGTAATTAAATGGAACAACAGTATGAATCTTCATCTG
TXA-1B3 1 -----
ATRX ORF 3041 ATGGCACTGAAAAGTTACCTGAGCGAGAAGAAATTTGTCATTTTCTAAGGGCATAAAACAAATTAAGAATGGAACAAC
TXA-1B3 1 -----
ATRX ORF 3121 GATGGAGAAAAGAAAAGTAAAAAATAAGAGATAAACTTCTAAAAAGAAGGATGAATTATCTGATTATGCTGAGAAGTC
TXA-1B3 1 -----
ATRX ORF 3201 AACAGGGAAGGAGATAGTTGTGACTCTTCAGAGGATAAAAAGAGTAAGAATGGAGCATATGGTAGAGAGAAGAAAAGGT
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ATRX ORF 3281 GCAAGTTGCTTGAAAGAGTTCAAGGAAGAGACAAGATTGCTCATCATCTGATACTGAGAAATATCCATGAAAGAAGAT
TXA-1B3 1 -----
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TXA-1B3 1 -----
ATRX ORF 3441 GGAAATACAAAGTGGCTCATCATCATCTGATGCTGAGGAAAGTTCTGAAGATAATAAAAGAAGAAGCAAAGAAGCTTCAT
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TXA-1B3 1 -----
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TXA-1B3 1 -----
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ATRX ORF 3761 TGCCTGTCACAGTGGATGATGATGATGACGACAATGATCCTGAGAATAGAATTGCCAAGAAGATGCTTTTAGAAGAAATT
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TXA-1B3 1 -----
ATRX ORF 3921 TGAAGAAAACCCAGGAGATGAGGAAGCAAAAATCAAGTCAATTCTGAATCAGATTCAGATTCTGAAGAATCTAAGAAGC
TXA-1B3 1 -----
ATRX ORF 4001 CAAGATACAGACATAGGCTTTTGCGGCACAAATTGACTGTGAGTGACGGAGAATCTGGAGAAGAAAAAAGACAAGCCT
TXA-1B3 1 -----
ATRX ORF 4081 AAAGAGCATAAAGAAGTCAAAGGCAGAAACAGAAGAAAGGTGAGCAGTGAAGATTGAGAAGATTCTGATTTTCAGGAATC
TXA-1B3 1 -----
ATRX ORF 4161 AGGAGTTAGTGAAGAAGTTAGTGAATCCGAAGATGAACAGCGGCCAGAACCAAGGTCTGCAAAGAAGCAGAGTTGGAAG
TXA-1B3 1 -----
ATRX ORF 4241 AAAATCAGCGGAGCTATAAACAGAAAAAGAAAAGGCGACGTATTAAGGTTCAAGAAGATTTCACAGTGA AAAACAAGAGT
TXA-1B3 1 -----
ATRX ORF 4321 AATTCTGAGGAAGAAGAGGAGGAAAAAGAAGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAAGATGAAAA
TXA-1B3 1 -----
ATRX ORF 4401 TGATGATTCCAAGTCTCCTGGAAAAGGCAGAAAGAAAATTCGGAAGATTCTTAAAGATGATAAACTGAGAACAGAAACAC
TXA-1B3 1 -----
ATRX ORF 4481 AAAATGCTCTTAAGGAAGAGGAAGAGAGACGAAAACGTATTGCTGAGAGGGAGCGTGAGCGAGAAAAATTGAGAGAGGTG
TXA-1B3 1 -----
ATRX ORF 4561 ATAGAAATTGAAGATGCTTCACCCACCAAGTGTCCAATAACAACCAAGTTGGTTTTAGATGAAGATGAAGAAACCAAAGA
TXA-1B3 1 -----
ATRX ORF 4641 ACCTTTAGTGCAGGTTTCATAGAAATATGGTTATCAAATTGAAACCCCATCAAGTAGATGGTGTTCAGTTTATGTGGGATT
TXA-1B3 1 -----
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TXA-1B3 1 -----
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TXA-1B3 1 -----
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TXA-1B3 1 -----
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TXA-1B3 1 -----
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TXA-1B3 1 -----
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TXA-1B3 1 -----

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ATRX ORF 5681 TTAGCAAAGAAAATAAGGGTTATTTTGTATGAAGACAGTATGGATGAATTTATAGCCTCAGATTCTGATGAAACCTCCATG
TXA-1B3 1 -----

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TXA-1B3 1 -----

ATRX ORF 5841 CAGTGACAATGATGTTGAAGTGATTAAGGTCTGGAATTCAAGATCTCGGGGAGGTGGTGAAGGAAATGTGGATGAAACAG
TXA-1B3 1 -----

ATRX ORF 5921 GAAACAATCCTTCTGTTTCTTTAAAACTGGAAGAAAGTAAAGCTACTTCTTCTTAATCCAAGCAGCCCAGCTCCAGAC
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ATRX ORF 6081 TCGAATGGCAGAGGAAATTGGGGATAAAGTCCTTGTTTTCAGCCAGTCCCTCATATCTCTGGACTTGATTGAAGATTTTC
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ATRX ORF 6161 TTGAATTAGCTAGTAGGGAGAAGACAGAAGATAAAGATAAACCCCTTATTTATAAAGGTGAGGGGAAGTGGCTTCGAAAC
TXA-1B3 1 -----

ATRX ORF 6241 ATTGACTATTACCGTTTAGATGGTTCCACTACTGCACAGTCAAGGAAGAAGTGGGCTGAAGAATTAATGATGAAACTAA
TXA-1B3 1 -----

ATRX ORF 6321 TGTGAGAGGACGATTATTTATCATTCTACTAAAGCAGGATCTCTAGGAATTAATCTGGTAGCTGCTAATCGAGTAATTA
TXA-1B3 1 -----

ATRX ORF 6401 TATTTCGACGCTTCTTGGAAATCCATCTTATGACATCCAGAGTATATTAGAGTTTATCGCTTTGGACAAACTAAGCCTGTT
TXA-1B3 1 -----

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TXA-1B3 1 -----

ATRX ORF 6561 TCGAGTTGTTGATCAGCAGCAGGTGGAGCGTCATTTACTATGAATGAGCTTACTGAACTTTATACTTTTGAGCCAGACT
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ATRX ORF 6641 TATTAGATGACCCTAATTCAGAAAAGAAGAAGAAGAGGGATACTCCCATGCTGCCAAAGGATACCATACTTGCAGAGCTC
TXA-1B3 1 -----

ATRX ORF 6721 CTTAGATACATAAAGAACACATTGTAGGATACCATGAACATGATTCTCTTTGGACCACAAAGAAGAAGAGTTGAC
TXA-1B3 1 -----

ATRX ORF 6801 TGAAGAAGAAAGAAAAGCAGCTTGGGCTGAGTATGAAGCAGAGAAGAAGGTACTGACCATGCGTTTCAACATACCAACTG
TXA-1B3 1 -----

ATRX ORF 6881 GGACCAATTTACCCCCTGTCAGTTTCAACTCTCAAACCTCTTATATTCTTTCAATTGGGAGCCCTGTCAGCAATGAGT
TXA-1B3 1 -----

ATRX ORF 6961 AATCAACAGCTGGAGGACCTCATTAATCAAGGAAGAGAAAAAGTTGTAGAAGCAACAACAGTGTGACAGCAGTGAGGAT
TXA-1B3 1 -----

ATRX ORF 7041 TCAACCTCTTGAGGATATAATTTAGCTGTATGGAAGGAGAACATGAATCTCTCAGAGGCCCAAGTACAGGCGTTAGCAT
TXA-1B3 1 -----

ATRX ORF 7121 TAAGTAGACAAGCCAGCCAGGAGCTTGATGTTAAACGAAGAGAAGCAATCTACAATGATGTATTGACAAAACAACAGATG
TXA-1B3 1 -----AGATG
AGATG

ATRX ORF 7201 TTAATCAGCTGTGTTTCAGCGAATACTTATGAACAGAAAGGCTCCAGCAGCAGTACAATCAGCAGCAACAGCAACAAATGAC
TXA-1B3 6 TTAATCAGCTGTGTTTCAGCGAATACTTATGAACAGAAAGGCTCCAGCAGCAGTACAATCAGCAGCAACAGCAACAAATGAC

ATRX ORF 7281 TTATCAACAAGCAACACTGGGTCACCTCATGATGCCAAGGCCCCAAATTTGATCATGAATCCTTCTAATACCAGCAGA
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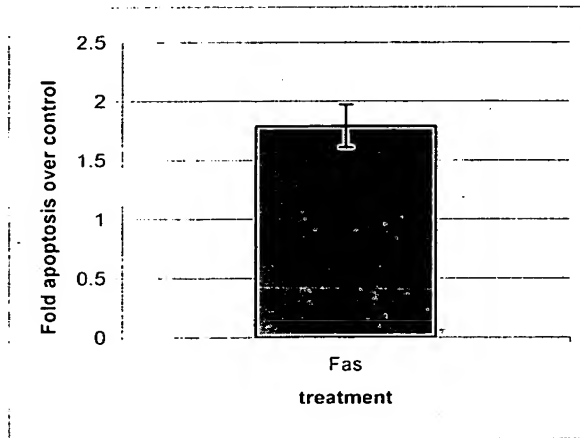
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TXA-1B3 166 TTGATATGAGAGGAATGTATCAGCCAGTGGCTGGTGGTATGCCAGCCACCATTACAGCGTGCACCACCCCAATGAGA

ATRX ORF 7441 AGCAAAAATCCAGGACCTTCCCAAGGGAAATCAATGTGA-----
TXA-1B3 246 AGCAAAAATCCAGGACCTTCCCAAGGGAAATCAATGTATTGCACTAAAGC

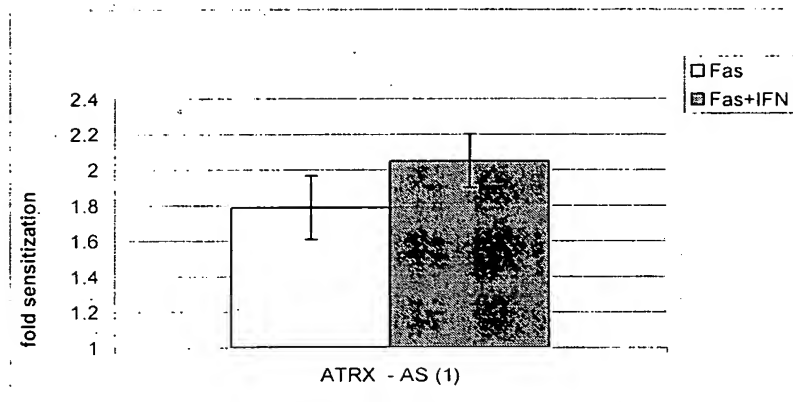
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Figure 4:
Validation of the anti-apoptotic effect of ATRX

a) AS fragment No. 1 (HAP-66D4) LOF results



b)



c) AS fragment No. 2 (TXA_1B3) LOF results

